WEST Search History

DATE: Thursday, March 21, 2002

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,PGPB; PLUR=YES; OP=ADJ			
L11	l10 and l7	1	L11
L10	(dna or cdna or nucleic acid or polynucleotide) and l9	4	L10
L9	(corynebacteria or corynebacteria glutamicum) and l8	4	L9
L8	Methyltetrahydrofolate homocysteine methyltransferase or Methionine synthase or Methionine synthetase	73	L8
L7	l6 or l5 or l4 or l3 or l2 or l1	13523	L7
L6	(((536/23.2)!.CCLS.))	3444	L6
L5	(((435/320.1)!.CCLS.))	10692	L5
L4	(((435/252.32)!.CCLS.))	110	L4
L3	(((435/252.3)!.CCLS.))	5269	L3
L2	(((435/193)!.CCLS.))	813	L2
L1	((435/183)!.CCLS.)	1248	L1

END OF SEARCH HISTORY

WEST

End of Result Set

Generate Collection Print

L11: Entry 1 of 1 File: USPT Feb 19, 2002

US-PAT-NO: 6348328
DOCUMENT-IDENTIFIER: US 6348328 B1

TITLE: Compounds

DATE-ISSUED: February 19, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Black; Michael Terence	Chester Springs	PA		
Hodgson; John Edward	Malvern	PA		
Knowles; David Justin Charles	Boroughbridge			GBX
Nicholas; Richard Oakley	Collegeville	PA		
Stodola; Robert King	Flourtown	PA		

ASSIGNEE-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY	TYPE CODE
SmithKline Beecham Corporation	Philadelphia	PA			02
SmithKline Beecham plc.				GBX	03

APPL-NO: 8/ 858207 [PALM]
DATE FILED: May 14, 1997

INT-CL: [7] C12 P 21/02

US-CL-ISSUED: 435/69.1; 435/320.1, 435/252.3, 536/23.1, 536/23.7
US-CL-CURRENT: 435/69.1; 435/252.3, 435/320.1, 536/23.1, 536/23.7

FIELD-OF-SEARCH: 536/23.4, 536/23.2, 536/23.7, 536/23.1, 435/253.3, 435/252.35, 435/320.1, 435/69.1

PRIOR-ART-DISCLOSED:

U.S. PATENT DOCUMENTS

Search Selected Search ALL

	PAT-NO	ISSUE-DATE	PATENTEE-NAME	US-CL
☐	5753480	May 1998	Lawlor	435/183
☐	5756330	May 1998	Lawlor	435/183
☐	5863777	January 1999	Lawlor	435/183

FOREIGN PATENT DOCUMENTS

FOREIGN-PAT-NO	PUBN-DATE	COUNTRY	US-CL
9610647	April 1996	WOX	

OTHER PUBLICATIONS

Critical Synergy: The Biotechnology Industry and Intellectual Property Protection, Biotechnology Industry Organization, Washington, D.C., 1994, pp. 75 and 100-107.

ART-UNIT: 1632
PRIMARY-EXAMINER: Martinell; James
ATTY-AGENT-FIRM: Gimmi; Edward R. Deibert; Thomas S. King; William T.

ABSTRACT:

This invention relates to newly identified polynucleotides, polypeptides encoded by such polynucleotides, the uses of such polynucleotides and polypeptides, as well as the production of such polynucleotides and polypeptides and recombinant host cells transformed with the polynucleotides. This invention also relates to inhibiting the biosynthesis or action of such polynucleotides or polypeptides and to the use of such inhibitors in therapy.

22 Claims, 0 Drawing figures

WEST

Generate Collection | Print

Search Results - Record(s) 1 through 4 of 4 returned.

☐ 1. Document ID: US 6348328 B1

L10: Entry 1 of 4 File: USPT Feb 19, 2002

US-PAT-NO: 6348328
DOCUMENT-IDENTIFIER: US 6348328 B1

TITLE: Compounds

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. Desc | Image

☐ 2. Document ID: US 6228983 B1

L10: Entry 2 of 4 File: USPT May 8, 2001

US-PAT-NO: 6228983
DOCUMENT-IDENTIFIER: US 6228983 B1

TITLE: Human respiratory syncytial virus peptides with antifusogenic and antiviral activities

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. Desc | Image

☐ 3. Document ID: US 6017536 A

L10: Entry 3 of 4 File: USPT Jan 25, 2000

US-PAT-NO: 6017536
DOCUMENT-IDENTIFIER: US 6017536 A

TITLE: Simian immunodeficiency virus peptides with antifusogenic and antiviral activities

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. Desc | Image

☐ 4. Document ID: US 5872104 A

L10: Entry 4 of 4 File: USPT Feb 16, 1999

US-PAT-NO: 5872104
DOCUMENT-IDENTIFIER: US 5872104 A

TITLE: Combinations and methods for reducing antimicrobial resistance

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc | Image

Generate Collection | Print

Terms	Documents
(dna or cdna or nucleic acid or polynucleotide) and l9	4

Display Format: - Change Format

Previous Page Next Page

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=> d his

     (FILE 'HOME' ENTERED AT 14:10:14 ON 21 MAR 2002)

     FILE 'REGISTRY' ENTERED AT 14:10:21 ON 21 MAR 2002
L1             1 S 9033-23-2/RN

     FILE 'HCAPLUS' ENTERED AT 14:13:37 ON 21 MAR 2002

     FILE 'REGISTRY' ENTERED AT 14:13:46 ON 21 MAR 2002
                SET SMARTSELECT ON
L2           SEL L1 1- CHEM :       15 TERMS
                SET SMARTSELECT OFF

     FILE 'HCAPLUS' ENTERED AT 14:13:47 ON 21 MAR 2002
L3           884 S L2
L4             0 S L3 (L) (CORYNEBACTERIA OR CORYNEBACTERIA GLUTAMICUM)
L5            93 S L3 (L) (DNA OR CDNA OR NUCLEIC ACID OR POLYNUCLEOTIDE)
L6            80 S L5 AND PD<20000802
```

=> d ibib ab 1-12

L6 ANSWER 1 OF 80 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:94757 HCAPLUS
DOCUMENT NUMBER: 135:176324
TITLE: Embarking on rice functional genomics via cDNA microarray: use of 3' UTR probes for specific gene expression analysis
AUTHOR(S): Yazaki, Junshi; Kishimoto, Naoki; Nakamura, Keiko; Fujii, Fumiko; Shimbo, Kanako; Otsuka, Yoshimi; Wu, Jianzhong; Yamamoto, Kimiko; Sakata, Katsumi; Sasaki, Takuji; Kikuchi, Shoshi
CORPORATE SOURCE: Institute of the Society for Techno-innovation of Agriculture, Forestry and Fisheries, Tsukuba, 305-0854, Japan
SOURCE: DNA Research (**2000**), 7(6), 367-370
CODEN: DARSE8; ISSN: 1340-2838
PUBLISHER: Universal Academy Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB EST mapping anal. revealed that primers designed from the 3' portion (3'-UTR) of rice ESTs were more gene specific than that from the 5' portion. This observation suggests that the full-length EST insert is effective for comprehensive anal. of family gene expression while the 3'-UTR probe is useful for detecting gene-specific expression. In the full-insert microarray, the ten most highly expressed genes consist of five ubiquitin homologs, two unknown genes and one homolog each of S-adenosyl **methionine synthase**, NADH dehydrogenase and actin. In the 3'-UTR microarray, three ubiquitin homologs, four unknown genes and one homolog each of thioredoxin, phenylalanine ammonia-lyase and methyltransferase showed the highest signals. Only three ubiquitin homologs and two unknown genes, however, were highly expressed in both full-insert and 3'-UTR microarrays. A 3'-UTR microarray is effective in detecting specific genes in target RNA from various tissues and at different developmental stages. A rice **cDNA** microarray with approx. 9000 ESTs were constructed. Information on the **cDNA** clones including identity and accession no. can be accessed at http://microarray.rice.**dna**.affrc. go.jp/.
REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 2 OF 80 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:35443 HCAPLUS
DOCUMENT NUMBER: 134:365268
TITLE: Co-morbidity of 5,10-methylenetetrahydrofolate reductase and methionine synthase gene polymorphisms and risk for neural tube defects
AUTHOR(S): Johanning, Gary L.; Tamura, T.; Johnston, Kelley E.; Wenstrom, Katharine D.
CORPORATE SOURCE: Department of Nutrition Sciences, The University of Alabama at Birmingham, Birmingham, AL, 35294-3360, USA
SOURCE: Journal of Medical Genetics (**2000**), 37(12), 949-951
CODEN: JMDGAE; ISSN: 0022-2593
PUBLISHER: BMJ Publishing Group
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Neural tube defects (NTD5) are among the most common and devastating birth defects. The gene for human **methionine synthase** (MS), which catalyzes the reaction to form methionine from homocysteine, has recently been cloned, and a common polymorphism has also been identified. Although MS plays an important role in homocysteine metab., this polymorphism has not been reported to be a risk factor for NTD formation, and, to our knowledge, comorbidity of MTHFR and MS polymorphisms for NTDs has never been evaluated. We detd. MTHFR and MS genotypes using **DNA** isolated from amniotic fluid cells of fetuses with NTDs and of those without any apparent malformations, and evaluated potential assocns.

between polymorphisms in these two genes as a risk factor for the development of NTDs. To our knowledge, this is the first reported study of interactions between frequently occurring polymorphisms of two genes involved in folate metab. We did not find strong assocns. between MTHFR and MS polymorphisms and the risk of NTDs.

REFERENCE COUNT: 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 3 OF 80 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:13837 HCAPLUS
DOCUMENT NUMBER: 135:223334
TITLE: Methionine synthase, a gene required for methionine synthesis, is expressed in planta by Cladosporium fulvum
AUTHOR(S): Solomon, Peter S.; Nielsen, Peter Stein; Clark, Anthony J.; Oliver, Richard P.
CORPORATE SOURCE: Department of Physiology, Carlsberg Laboratory, Valby, DK-2500, Den.
SOURCE: Molecular Plant Pathology (**2000**), 1(5), 315-323
CODEN: MPPAFD; ISSN: 1464-6722
PUBLISHER: Blackwell Science Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The nutritional requirements of phytopathogenic fungi growing in planta has to date been largely ignored. We have begun to address this problem by investigating the methionine requirement for the biotrophic pathogen of tomato Cladosporium fulvum during infection. The Met6 gene from Cladosporium fulvum encoding a cobalamin-independent 5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase, was cloned by functional yeast complementation. The open reading frame was found to be 2304 bp, contg. no introns and encoding a protein of 87 kDa. In vitro Northern anal. demonstrated high levels of Met6 expression in the absence of externally supplied methionine. However in the presence of methionine or in the absence of carbon, expression of Met6 decreased significantly. Anal. of Met6 expression in planta revealed a strong increase during infection suggesting the requirement for methionine synthesis in planta by Cladosporium fulvum. This study demonstrates that Cladosporium fulvum is starving for methionine during infection and thus implies the essentiality of primary biosynthetic pathways to the infecting fungus.

REFERENCE COUNT: 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 4 OF 80 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:886027 HCAPLUS
DOCUMENT NUMBER: 134:309023
TITLE: Reduced mRNA abundance of the main enzymes involved in methionine metabolism in human liver cirrhosis and hepatocellular carcinoma
AUTHOR(S): Avila, Matias A.; Berasain, Carmen; Torres, Luis; Martin-Duce, Antonio; Corrales, Fernando J.; Yang, Heping; Prieto, Jesus; Lu, Shelly C.; Caballeria, Juan; Rodes, Juan; Mato, Jose M.
CORPORATE SOURCE: Division de Hepatologia y Terapia Genica, Departmento de Medicina Interna, Universidad de Navarra, Pamplona, 31008, Spain
SOURCE: Journal of Hepatology (**2000**), 33(6), 907-914
CODEN: JOHEEC; ISSN: 0168-8278
PUBLISHER: Munksgaard International Publishers Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB It has been known for at least 50 yr that alterations in methionine metab. occur in human liver cirrhosis. However, the mol. basis of this alteration is not completely understood. To gain more insight into the mechanisms behind this condition, mRNA levels of methionine adenosyltransferase (MAT1A), glycine methyltransferase (GNMT),

methionine synthase (MS), betaine homocysteine methyltransferase (BHMT) and cystathionine .beta.-synthase (CBS) were examd. in 26 cirrhotic livers, five hepatocellular carcinoma (HCC) tissues, and ten control livers. The expression of the above-mentioned genes was detd. by quant. RT-PCR anal. Methylation of MAT1A promoter was assessed by methylation-sensitive restriction enzyme digestion of genomic **DNA**. When compared to normal livers MAT1A, GNMT, BHMT, CBS, and MS mRNA contents were reduced in liver cirrhosis. Interestingly, MAT1A promoter was hypermethylated in the cirrhotic liver. HCC tissues also showed decreased mRNA levels of these enzymes. Thus, the abundance of the mRNA of the main genes involved in methionine metab. is markedly reduced in human cirrhosis and HCC. Hypermethylation of MAT1A promoter could participate in its reduced expression in cirrhosis. These observations help to explain the hypermethioninemia, hyperhomocysteinemia and reduced hepatic glutathione content obsd. in cirrhosis.

REFERENCE COUNT: 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 5 OF 80 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2000:858338 HCAPLUS

DOCUMENT NUMBER: 134:278671

TITLE: Methyl group metabolism gene polymorphisms and susceptibility to prostatic carcinoma

AUTHOR(S): Kimura, Fumihiro; Franke, Knut H.; Steinhoff, Christine; Golka, Klaus; Roemer, Hermann C.; Anastasiadis, Aristoteles G.; Schulz, Wolfgang A.

CORPORATE SOURCE: Urologische Klinik, Heinrich Heine Universitat, Dusseldorf, D-40225, Germany

SOURCE: Prostate (New York) (**2000**), 45(3), 225-231
CODEN: PRSTDS; ISSN: 0270-4137

PUBLISHER: Wiley-Liss, Inc.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Alterations of **DNA** methylation are very frequent in prostatic carcinoma. A possible cause underlying altered **DNA** methylation could be an insufficient level of S-adenosylmethionine as a consequence of nutritional imbalances or of weaker alleles of genes for its synthesis, i.e., encoding methylene-tetrahydrofolate reductase (MTHFR), **methionine synthase** (MS), and .beta.-cystathionine synthetase (CBS). Therefore, homozygosity or heterozygosity for such weaker alleles may underlie susceptibility to prostatic carcinoma. The distribution of the two most frequent MTHFR, MS, and CBS alleles was detd. in 132 prostatic carcinoma patients and 150 population controls by restriction fragment length polymorphism-(RFLP) PCR. In the controls, a Hardy-Weinberg equil. was obsd. for each allele pair. No significant differences were obsd. with respect to age or gender. No significant differences for single genes or combinations were found between prostatic carcinoma patients and controls, although the MTHFR Val allele was slightly overrepresented among the tumor patients. Neither did the allele distribution significantly differ among the prostatic carcinoma patients stratified according to age, clin. stage, or presence of metastases. However, the MTHFR Val allele tended to be assocd. with higher tumor grade. In general, the data do not support the hypothesis that weaker alleles in Me group metab. genes constitute a major factor in the high prevalence of **DNA** methylation alterations found in prostatic carcinoma. However, a potential assocn. with the MTHFR genotype deserves further study.

REFERENCE COUNT: 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 6 OF 80 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2000:812999 HCAPLUS

DOCUMENT NUMBER: 135:1051

TITLE: Analysis of the methionine biosynthetic pathway in the extremely thermophilic eubacterium Thermus thermophilus

AUTHOR(S): Kosuge, Takehide; Gao, Dai; Hoshino, Takayuki

CORPORATE SOURCE: Institute of Applied Biochemistry, University of Tsukuba, Tsukuba, 305-8572, Japan
SOURCE: Journal of Bioscience and Bioengineering (**2000**), 90(3), 271-279
CODEN: JBBIF6; ISSN: 1389-1723
PUBLISHER: Society for Bioscience and Bioengineering, Japan
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Four **DNA** fragments that could rescue the mutations of four Met- mutants were cloned from Thermus thermophilus HB27 and their complete nucleotide sequences were detd. Two of the four fragments resp. contained the greater parts of the metF and metH genes, the predicted amino acid sequences of which showed identities of 30.8% and 32.7% with 5,10-methylenetetrahydrofolate reductase (E.C. 1.7.99.5) and vitamin B12-dependent homocysteine transmethylase (**E.C. 2.1.1.13**) of Escherichia coli. The other two **DNA** fragments, which overlapped one another, contained two open reading frames whose predicted amino acid sequences were resp. similar to those of O-acetylhomoserine sulfhydrylase (E.C. 4.2.99.10, the product of the MET17 gene) and homoserine O-acetyltransferase (E.C. 2.3.1.31, the product of the MET2 gene) of Saccharomyces cerevisiae. The metF, metH, MET2, and MET17 genes of T. thermophilus were disrupted by introducing the heat-stable kanamycin nucleotidyltransferase gene into the genome. Each transformant showed methionine auxotrophy. Both the MET2- and MET17-disrupted mutants could grow in a minimal medium contg. homocysteine but not in the same medium contg. succinylhomoserine or cystathionine. In contrast, the metF- and metH-disrupted mutants could not grow in the minimal medium contg. homocysteine. These results suggest that in T. thermophilus, homoserine is directly converted to homocysteine via O-acetylhomoserine and that homocysteine is methylated to synthesize methionine.

REFERENCE COUNT: 51 THERE ARE 51 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 7 OF 80 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:763256 HCAPLUS
DOCUMENT NUMBER: 134:40298
TITLE: Defects in methylthioadenosine phosphorylase are associated with but not responsible for methionine-dependent tumor cell growth
AUTHOR(S): Tang, Baiqing; Li, Yunan N.; Kruger, Warren D.
CORPORATE SOURCE: Division of Population Science, Fox Chase Cancer Center, Philadelphia, PA, 19111, USA
SOURCE: Cancer Research (**2000**), 60(19), 5543-5547
CODEN: CNREA8; ISSN: 0008-5472
PUBLISHER: American Association for Cancer Research
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A large proportion of human tumor-derived cell lines and primary tumor cells show methionine-dependent growth. This phenomenon refers to the ability of cells to grow in media contg. methionine and the inability of cells to grow in media supplemented with methionine's precursor, homocysteine (Hcy). Methionine can be formed by two different pathways, the recycling pathway and the salvage pathway. To discover the basis for methionine-dependent growth, the authors have analyzed 12 tumor cell lines and 2 non-tumor-derived cell lines for defects in two key genes in different methionine synthetic pathways. The authors found little evidence that defects in **methionine synthase** expression or mutations in the MS gene are correlated with methionine-dependent growth. However, the authors did find a correlation between methionine-dependent growth and defects in expression of methylthioadenosine phosphorylase (MTAP), a key enzyme in the salvage pathway. Three of the four cell lines lacking detectable MTAP protein were unable to grow in Hcy-contg. media, whereas all six of the MTAP-pos. cell lines tested showed strong growth. However, when the authors introduced MTAP **cDNA** into MTAP-deficient MCF-7 cells, the resulting cell line was still defective in growth on Hcy, although it

could now grow on the salvage pathway precursor methylthioadenosine. These findings indicate that salvage pathway defects are not causally related to methionine-dependent growth.

REFERENCE COUNT: 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 8 OF 80 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:753687 HCAPLUS
DOCUMENT NUMBER: 134:205650
TITLE: Molecular biology of methionine synthase: Interrelationships with homocysteine and vascular disease
AUTHOR(S): Banerjee, Ruma
CORPORATE SOURCE: Biochemistry Department, University of Nebraska, Lincoln, NE, 68588-0664, USA
SOURCE: Developments in Cardiovascular Medicine (**2000**), 230, 291-311
CODEN: DCMEDM; ISSN: 0166-9842
PUBLISHER: Kluwer Academic Publishers
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review, with 66 refs. **Methionine synthase** is one of two key enzymes that manages cellular homocysteine and is found in most mammalian tissues. It catalyzes the B12-dependent transmethylation of homocysteine using methyltetrahydrofolate as a Me group donor. The **cDNA** encoding human **methionine synthase** has been cloned recently and its sequence has been detd. Catastrophic mutations in **methionine synthase** are found in the cblG class of patients, and are correlated with severe hyperhomocysteinemia with attendant cardiovascular diseases. However, polymorphisms have yet to be found that are correlated with the moderate hyperhomocysteinemia. A mouse knock out of the **methionine synthase** gene confers an embryonic lethal phenotype, indicating that it is an essential gene. The activity of **methionine synthase** is also dependent on redox proteins that reactivate oxidized enzyme. The components of this redox pathway have been described recently to be a cytochrome P450-like **methionine synthase** reductase and sol. cytochrome b5. Mutations in **methionine synthase** reductase have been identified in the cblE class of patients and are correlated with severe hyperhomocysteinemia.

REFERENCE COUNT: 66 THERE ARE 66 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 9 OF 80 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:728565 HCAPLUS
DOCUMENT NUMBER: 134:261672
TITLE: MET15 as a visual selection marker for Candida albicans
AUTHOR(S): Viaene, Jasmine; Tiels, Petra; Logghe, Marc; Dewaele, Sylviane; Martinet, Wim; Contreras, Roland
CORPORATE SOURCE: Department of Molecular Biology, Unit of Fundamental and Applied Molecular Biology, University of Ghent and Flanders Interuniversity Institute for Biotechnology, Ghent, B-9000, Belg.
SOURCE: Yeast (**2000**), 16(13), 1205-1215
CODEN: YESTE3; ISSN: 0749-503X
PUBLISHER: John Wiley & Sons Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB To develop better mol. genetic tools for the diploid yeast Candida albicans, the suitability of the MET15 gene as a visual selection marker was studied. Both MET15 alleles of C. albicans CAI-4 were isolated by functional complementation of a Saccharomyces cerevisiae strain lacking the MET15 gene. Growth of this complemented strain on Pb2+-contg. medium was assocd. with a color shift of brown into white colonies. The MET15 alleles of C. albicans were located on chromosome 4 by pulsed-field gel electrophoresis and Southern blotting. A met15-deficient strain of C.

albicans CAI-4 was generated using the ura blaster technique. This strain showed a brown colony color on Pb2+-contg. medium, which corresponded with the colony color of a S. cerevisiae strain lacking the MET15 gene. Unexpectedly, the met15-deficient strain of C. albicans still grew on methionine-depleted medium. However, this growth was severely delayed. In addn., complementation of this strain with an integrative or replicative plasmid contg. either of the MET15 alleles resulted in the formation of white transformants on Pb2+-contg. medium. These transformants grew very well on methionine-depleted medium. Colony sectoring was obtained with the replicative plasmid and not with the integrative one. This study demonstrates that the MET15 gene of C. albicans is suitable as a visual marker and therefore can be used to identify transformants and study plasmid stability.

REFERENCE COUNT: 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 10 OF 80 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:709207 HCAPLUS
DOCUMENT NUMBER: 134:160885
TITLE: Genetic modulation of homocysteinemia
AUTHOR(S): Rozen, Rima
CORPORATE SOURCE: Departments of Human Genetics, Pediatrics, and Biology, McGill University, Montreal Children's Hospital, Montreal, Can.
SOURCE: Seminars in Thrombosis and Hemostasis (**2000**), 26(3), 255-261
CODEN: STHMBV; ISSN: 0094-6176
PUBLISHER: Thieme Medical Publishers, Inc.
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English

AB A review with 57 refs. With the identification of hyperhomocysteinemia as a risk factor for cardiovascular disease, an understanding of the genetic determinants of plasma homocysteine is important for prevention and treatment. It has been known for some time that homocystinuria, a rare inborn error of metab., can be due to genetic mutations that severely disrupt homocysteine metab. A more recent development is the finding that milder, but more common, genetic mutations in the same enzymes might also contribute to an elevation in plasma homocysteine. The best example of this concept is a missense mutation (alanine to valine) at base pair (bp) 677 of methylenetetrahydrofolate reductase (MTHFR), the enzyme that provides the folate deriv. for conversion of homocysteine to methionine. This mutation results in mild hyperhomocysteinemia, primarily when folate levels are low, providing a rationale (folate supplementation) for overcoming the genetic deficiency. Addnl. genetic variants in MTHFR and in other enzymes of homocysteine metab. are being identified as the **cDNAs**/genes become isolated. These variants include a glutamate to alanine mutation (bp 1298) in MTHFR, an aspartate to glycine mutation (bp 2756) in **methionine synthase**, and an isoleucine to methionine mutation (bp 66) in **methionine synthase** reductase. These variants have been identified relatively recently; therefore addnl. investigations are required to det. their clin. significance with respect to mild hyperhomocysteinemia and vascular disease.

REFERENCE COUNT: 57 THERE ARE 57 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 11 OF 80 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:590906 HCAPLUS
DOCUMENT NUMBER: 133:279864
TITLE: The Allele Frequency of Mutations in Four Genes that Confer Enhanced Susceptibility to Venous Thromboembolism in an Unselected Group of New York State Newborns
AUTHOR(S): Conroy, J. M.; Trivedi, G.; Sovd, T.; Caggana, M.
CORPORATE SOURCE: P.O. Box 509, Wadsworth Center, Division of Genetic Disorders, Molecular Genetic Epidemiology Laboratory, New York State Department of Health, Albany, NY,

12201-0509, USA
SOURCE: Thromb. Res. (**2000**), 99(4), 317-324
CODEN: THBRAA; ISSN: 0049-3848
PUBLISHER: Elsevier Science Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The frequencies of Factor V G1691A (FV Leiden, FVL), prothrombin (PT) G20210A, 5',10'-methylenetetrahydrofolate reductase (MTHFR) C677T, and **methionine synthase** (MS) A2756G (four mutations assocd. with an increased risk of venous thromboembolism [VTE]) were detd. in a sample of approx. 1500 New York State residents. Dried blood spots from approx. equal nos. of Caucasians, African-Americans and Hispanics were anonymously obtained from the New York State Department of Health Newborn Screening Program. Following PCR amplification of dried blood spot **DNA**, allele-specific oligonucleotide hybridization was used to detect mutant alleles. The total no. of individuals at increased genetic risk for VTE was 271 (17.5%) of the 1553 persons tested. Increased genetic risk was defined as the heterozygous state for FVL or PT and the homozygous state for the MTHFR or MS polymorphisms. Sixteen individuals had more than one genetic risk factor. The MS gene variant allele frequencies for African-Americans and Hispanics are the first to be reported. This report also provides an est. of the variant PT allele in the largest group of Hispanics studied to date.
REFERENCE COUNT: 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 12 OF 80 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:493687 HCAPLUS
DOCUMENT NUMBER: 133:115929
TITLE: Human **methionine synthase** reductase and **cDNA** and methods for evaluating risk of neural tube defects, cardiovascular disease, cancer, and Down's syndrome
INVENTOR(S): Gravel, Roy A.; Rozen, Rima; Leclerc, Daniel; Wilson, Aaron; Rosenblatt, David
PATENT ASSIGNEE(S): McGill University, Can.
SOURCE: PCT Int. Appl., 85 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000042196	A2	20000720	WO 2000-IB209	20000114 <--
WO 2000042196	A3	20010125		

W: CA, JP
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

PRIORITY APPLN. INFO.: US 1999-232028 A 19990115
US 1999-371347 A 19990810

AB The invention features a novel **cDNA** encoding **methionine synthase** reductase. The invention also features a method for detecting an increased likelihood of hyperhomocysteinemia and, in turn, an increased or decreased likelihood of neural tube defects, cardiovascular disease, Down's Syndrome or cancer. The invention also features therapeutic methods for treating and/or reducing the risk of cardiovascular disease, Down's Syndrome, cancer, or neural tube defects. Also provided are the sequences of the human **methionine synthase** reductase gene and protein and compds. and kits for performing the methods of the invention. Thus, the **cDNA** for human **methionine synthase** reductase was cloned and sequenced. Northern blots indicated that the **methionine synthase** reductase gene was expressed to some degree in all tissues but is particularly abundant in skeletal muscle. In addn. to a 3.6 kb band, a 3.1 kb and a faint 6 kb band were detected in brain mRNA.

The **methionine synthase** reductase gene was mapped to human chromosome 5p15.2-p15.3. Two deletion mutations were found in cblE patients: one resulted in deletion of Ile-576, the other resulted in a frameshift and premature truncation. Two polymorphisms were also detected: a G/A polymorphism at nucleotide 66 resulting in either Ile or Met at position 22 and a second G/A polymorphism at nucleotide 110 resulting in Tyr or Cys at position 37. Correlation of **methionine synthase** reductase gene mutations and risk for neural tube defects, Down's syndrome, and premature coronary artery disease was examd.

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L1             1 9033-23-2/RN

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L1   ANSWER 1 OF 1  REGISTRY  COPYRIGHT 2002 ACS
RN   9033-23-2  REGISTRY
CN   Methyltransferase, methyltetrahydrofolate-homocysteine (9CI)  (CA INDEX
     NAME)
OTHER NAMES:
CN   Cobalamin-dependent methionine synthase
CN   E.C. 2.1.1.13
CN   Methionine synthase
CN   Methionine synthetase
CN   Methyltetrahydrofolate-homocysteine methyltransferase
CN   Methyltetrahydrofolate-homocysteine vitamin B12 methyltransferase
CN   N-Methyltetrahydrofolate:L-homocysteine methyltransferase
CN   N5-Methyltetrahydrofolate methyltransferase
CN   N5-Methyltetrahydrofolate-homocysteine methyltransferase
CN   N5-Methyltetrahydrofolic-homocysteine vitamin B12 transmethylase
CN   Tetrahydrofolate methyltransferase
CN   Tetrahydropteroylglutamate methyltransferase
CN   Tetrahydropteroylglutamic methyltransferase
CN   Vitamin B12 methyltransferase
MF   Unspecified
CI   MAN
LC   STN Files:   ADISNEWS, AGRICOLA, ANABSTR, BIOBUSINESS, BIOSIS, BIOTECHNO,
       CA, CAPLUS, CEN, CIN, EMBASE, PROMT, TOXCENTER, USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
             444 REFERENCES IN FILE CA (1967 TO DATE)
             445 REFERENCES IN FILE CAPLUS (1967 TO DATE)
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NiceZyme View of ENZYME: EC 2.1.1.13

Official Name
5-methyltetrahydrofolate--homocysteine S-methyltransferase.
Alternative Name(s)
Methionine synthase. Tetrahydropteroylglutamate methyltransferase.
Reaction catalysed
5-methyltetrahydrofolate + L-homocysteine <=> tetrahydrofolate + L-methionine
Cofactor(s)
Cobalamin.
Comments
• Acts on monoglutamate or triglutamate derivatives. • The bacterial enzyme requires S-adenosyl-L-methionine and reduced FAD.
Cross-References

BRENDA	2.1.1.13
EMP/PUMA	2.1.1.13
WIT	2.1.1.13
KYOTO UNIVERSITY LIGAND CHEMICAL DATABASE	2.1.1.13
IUBMB Enzyme Nomenclature	2.1.1.13
MEDLINE	Find literature relating to 2.1.1.13
SWISS-PROT	Q09582, METH_CAEEL; P13009, METH_ECOLI; Q99707, METH_HUMAN; Q49775, METH_MYCLE; O33259, METH_MYCTU; O33465, METH_PSEPU; P37586, METH_SALTY; Q55786, METH_SYNY3;

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